



1. An isolated CCR3 regulatory site comprising base pairs in an untranslated exon 1 of a human CCR3 gene or mRNA capable of binding to regulatory elements.

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2. The regulatory site of claim 1 comprising SEQ ID NO:16.
3. The regulatory site of claim 1 wherein the regulatory elements are binding sites for antisense oligonucleotides.
4. The regulatory site of claim 1 wherein the regulatory elements are binding sites for transcription factors.
5. The regulatory site of claim 4 wherein the transcription factors are at least one of GATA-1, GATA-2, GATA-3, AML-1a, and combinations thereof.
6. The regulatory site of claim 4 wherein said sites are at least one of SEQ ID NO:17, SEQ ID NO:18, and SEQ ID NO:19.
7. The regulatory site of claim 1 comprising SEQ ID NO:21.
8. The regulatory site of claim 3 wherein said sites are at least one of SEQ ID NO:22, SEQ ID NO:23, and SEQ ID NO:24.

9. A method for cell selective gene expression in a human comprising providing to said human a pharmaceutically acceptable formulation of at least one regulatory element for binding to an untranslated exon in a human cell containing a CCR3 gene or mRNA.

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10. The method of claim 9 wherein said element regulates transcription of at least one of exon 1, exon 2, and exon 3.

11. The method of claim 9 wherein said element regulates binding of a transcription factor.

12. The method of claim 9 wherein said element is selected from the group consisting of a transcription factor inhibitor, an antisense oligonucleotide, and combinations thereof.

13. The method of claim 12 wherein said element is an inhibitor for a GATA transcription factor.

14. The method of claim 12 wherein the cell is selected from the group consisting of a leukocyte, an epithelial cell, an endothelial cell, and combinations thereof.

15. A method of regulating expression of CCR3 comprising providing an inhibitor for a CCR3 exon 1 transcription factor to a human cell containing a CCR3 receptor.

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16. The method of claim 15 wherein the inhibitor binds to CCR3 exon 1 at a GATA binding site.

17. The method of claim 16 wherein the binding site comprises SEQ ID NO:16.

18. The method of claim 16 wherein the binding site is at least one of SEQ ID NO:17, SEQ ID NO:18, and SEQ ID NO:19.

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20. The regulatory site of claim 19 wherein the regulatory elements are selected from the group consisting of binding sites for antisense oligonucleotides, binding sites for transcription factors, and combinations thereof.

21. A method of regulating expression of CCR3 comprising providing at least one element to regulate untranslated exon 2 in a CCR3 gene or mRNA.

Country	Year	Population (millions)	Urban population (millions)	Urban population (%)	Population density (per sq km)	Urban population density (per sq km)
Algeria	1975	10.0	4.0	40.0	100	400
Algeria	1980	10.5	4.5	42.9	110	450
Algeria	1985	11.0	5.0	45.5	120	500
Algeria	1990	11.5	5.5	47.8	130	550
Algeria	1995	12.0	6.0	50.0	140	600
Algeria	2000	12.5	6.5	52.0	150	650
Algeria	2005	13.0	7.0	53.8	160	700
Algeria	2010	13.5	7.5	55.6	170	750
Algeria	2015	14.0	8.0	57.1	180	800
Algeria	2020	14.5	8.5	58.6	190	850
Algeria	2025	15.0	9.0	60.0	200	900
Algeria	2030	15.5	9.5	61.3	210	950
Algeria	2035	16.0	10.0	62.5	220	1000
Algeria	2040	16.5	10.5	63.6	230	1050
Algeria	2045	17.0	11.0	64.7	240	1100
Algeria	2050	17.5	11.5	65.7	250	1150
Algeria	2055	18.0	12.0	66.7	260	1200
Algeria	2060	18.5	12.5	67.6	270	1250
Algeria	2065	19.0	13.0	68.4	280	1300
Algeria	2070	19.5	13.5	69.2	290	1350
Algeria	2075	20.0	14.0	70.0	300	1400
Algeria	2080	20.5	14.5	70.7	310	1450
Algeria	2085	21.0	15.0	71.4	320	1500
Algeria	2090	21.5	15.5	72.1	330	1550
Algeria	2095	22.0	16.0	72.7	340	1600
Algeria	2100	22.5	16.5	73.3	350	1650
Algeria	2105	23.0	17.0	73.9	360	1700
Algeria	2110	23.5	17.5	74.5	370	1750
Algeria	2115	24.0	18.0	75.0	380	1800
Algeria	2120	24.5	18.5	75.5	390	1850
Algeria	2125	25.0	19.0	76.0	400	1900
Algeria	2130	25.5	19.5	76.5	410	1950
Algeria	2135	26.0	20.0	76.9	420	2000
Algeria	2140	26.5	20.5	77.3	430	2050
Algeria	2145	27.0	21.0	77.8	440	2100
Algeria	2150	27.5	21.5	78.2	450	2150
Algeria	2155	28.0	22.0	78.6	460	2200
Algeria	2160	28.5	22.5	78.9	470	2250
Algeria	2165	29.0	23.0	79.3	480	2300
Algeria	2170	29.5	23.5	79.7	490	2350
Algeria	2175	30.0	24.0	80.0	500	2400
Algeria	2180	30.5	24.5	80.3	510	2450
Algeria	2185	31.0	25.0	80.6	520	2500
Algeria	2190	31.5	25.5	81.0	530	2550
Algeria	2195	32.0	26.0	81.3	540	2600
Algeria	2200	32.5	26.5	81.6	550	2650
Algeria	2205	33.0	27.0	81.8	560	2700
Algeria	2210	33.5	27.5	82.1	570	2750
Algeria	2215	34.0	28.0	82.4	580	2800
Algeria	2220	34.5	28.5	82.6	590	2850
Algeria	2225	35.0	29.0	82.9	600	2900
Algeria	2230	35.5	29.5	83.1	610	2950
Algeria	2235	36.0	30.0	83.3	620	3000
Algeria	2240	36.5	30.5	83.6		



25. An isolated CCR3 regulatory site comprising base pairs in untranslated exon 3 of a CCR3 gene or mRNA capable of binding to regulatory elements.

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26. The regulatory site of claim 25 wherein the regulatory elements are selected from the group consisting of binding sites for antisense oligonucleotides, binding sites for transcription factors, and combinations thereof.

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28. The method of claim 27 wherein said element regulates transcription of untranslated exon 3.
29. The method of claim 27 wherein said element regulates binding of a transcription factor.
30. The method of claim 27 wherein said element is selected from the group consisting of a transcription factor inhibitor, an antisense oligonucleotide, and combinations thereof.

31. An isolated CCR3 regulatory site comprising base pairs in a promoter of a human CCR3 gene or mRNA capable of binding to regulatory elements.

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32. The regulatory site of claim 31 comprising SEQ ID NO:20.
33. The regulatory site of claim 31 wherein the regulatory elements are selected from the group consisting of binding sites for antisense oligonucleotides, binding sites for transcription factors, and combinations thereof.
34. The regulatory site of claim 33 wherein the transcription factors are selected from the group consisting of GATA-1, GATA-2, GATA-3, AML-1, C/EBP, and combinations thereof.

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36. The method of claim 35 wherein said element regulates transcription of at least one of exon 1, exon 2, exon 3, and exon 4.

37. The method of claim 35 wherein said element regulates binding of a transcription factor.

38. The method of claim 35 wherein said element is selected from the group consisting of a transcription factor inhibitor, an antisense oligonucleotide, and combinations thereof.

39. The method of claim 38 wherein said element is an inhibitor for a transcription factor selected from the group consisting of a GATA transcription factor, a C/EBP transcription factor, an AML-1 transcription factor, and combinations thereof.

40. An isolated complex of CCR3 exon 2 and an antisense oligonucleotide bound to at least one base pair in exon 2, said complex blocking mRNA accumulation.

41. An isolated complex of CCR3 exon 3 and an antisense oligonucleotide bound to at least one base pair in exon 3, said complex blocking mRNA accumulation.

42. An isolated nucleic acid regulatory site for human CCR3 expression comprising SEQ ID NO: 16.

43. The regulatory site of claim 42 selected from the group consisting of SEQ ID NO: 17, SEQ ID NO:18, SEQ ID NO:19, and combinations thereof.

43. The regulatory site of claim 42 selected from the group consisting of SEQ ID NO: 17, SEQ ID NO:18, SEQ ID NO:19, and combinations thereof.

44. An isolated nucleic acid regulatory site for human CCR3 expression comprising SEQ ID NO:21.

項目	単位	数	金額	備考
1. 雑費	雑費	100	100	
2. 雑費	雑費	100	100	
3. 雑費	雑費	100	100	
4. 雑費	雑費	100	100	
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79. 雑費	雑費	100	100	
80. 雑費	雑費	100	100	
81. 雑費	雑費	100	100	





46. A method for cell selective gene expression in a human comprising providing to said human a pharmaceutically acceptable formulation of at least one regulatory element for binding to an untranslated exon in a human cell containing a CCR3 gene or mRNA and an agent selected from the group consisting of an anti-sense oligonucleotide against IL-5, a humanized anti-IL-5 antibody, and combinations thereof.
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